

In the SpecificationPlease substitute the following paragraph on page 1, beginning at line 9:Cross-Reference to a Related Applications

This application is a continuation-in-part of ~~co-pending~~ U.S. Application No. 09/312,433, filed May 14, 1999, now U.S. Patent No. 6,403,863, which is a continuation-in-part of ~~co-pending~~ U.S. Application No. 08/972,545, filed November 18, 1997, now U.S. Patent No. 6,069,300. This ~~application also U.S. Application No. 09/312,433 claims priority from the benefit of~~ U.S. Provisional Application No. ~~60,085,460~~ 60/085,460, filed May 14, 1998 and U.S. Application No. 08/972,545 claims the benefit of U.S. Provisional Application No. 60/031,045, filed November 18, 1996.

Please substitute the following paragraph on page 5, beginning at line 14 through to page 6, line 2:

As Hannah and Nelson (Hannah, L.C., O.E. Nelson (1975) *Plant Physiol.* ~~55:297-302~~; 55:297-302; Hannah, L.C., and Nelson, Jr., O.E. [1976] *Biochem. Genet.* 14:547-560) postulated, both *Shrunken-2* (*Sh2*) (Bhave, M.R., S. Lawrence, C. Barton, L.C. Hannah [1990] *Plant Cell* 2:581-588) and *Brittle-2* (*Bt2*) (Bae, J.M., M. Giroux, L.C. Hannah [1990] *Maydica* 35:317-322) are structural genes of maize endosperm ADP-glucose pyrophosphorylase. *Sh2* and *Bt2* encode the large subunit and small subunit of the enzyme, respectively. From cDNA sequencing, *Sh2* and *Bt2* proteins have predicted molecular weight of 57,179 Da (Shaw, J.R., L.C. Hannah [1992] *Plant Physiol.* 98:1214-1216) and 52,224 Da, respectively. The endosperm is the site of most starch deposition during kernel development in maize. *Sh2* and ~~*bt2-Bt2*~~ maize endosperm mutants have greatly reduced starch levels corresponding to deficient levels of AGP activity. Mutations of either gene have been shown to reduce AGP activity by about 95% (Tsai and Nelson, 1966, *supra*; Dickinson and Preiss, 1969, *supra*). Furthermore, it has been observed that enzymatic activities increase with the dosage of functional wild type *Sh2* and *Bt2* alleles, whereas mutant enzymes have altered kinetic properties. AGP is the rate limiting step in starch biosynthesis in plants. Stark *et al.* placed a mutant form of *E. coli* AGP in potato tuber and obtained a 35% increase in starch content (Stark *et al.* [1992] *Science* 258:287).

Please substitute the following paragraphs on page 7, beginning on line 21 through to page 8, line 18:

Figure 2 shows primary sequence alignment of the region surrounding HS 33 mutation (SEQ ID NO:1) in the AGP large subunits for maize (SEQ ID NO:2), wheat (SEQ ID NO:3), barley (SEQ ID NO:4), and potato (SEQ ID NO:5). Conserved regions are boxed.

Figure 3 shows primary sequence alignment of the region surrounding HS 40 mutation (SEQ ID NO:6) in the AGP large subunits for maize (SEQ ID NO:7), wheat (SEQ ID NO:8), barley (SEQ ID NO:9), and potato (SEQ ID NO:10). Conserved regions are boxed. Bolded aspartic acid residue corresponds to D413A allosteric mutant of potato LS (Greene, T.W., Woodbury, R.L., and Okita, T.W. [1996] *Plant Physiol.* (112:1315-1320). Spinach leaf AGP sequence (SEQ ID NO:11) is the activator site 2 peptide identified in 3-PGA analogue studies (Ball, K. and Preiss, J. [1994] *J. Biol. Chem.* 269:24706-24711). The labeled lysine residue is bolded.

Figures 4A and 4B show molecular characterization of TS48 (SEQ ID NO:12) and TS60 (SEQ ID NO:17), respectively. Genetic lesion of TS48 (SEQ ID NO:12) and corresponding residues are in bold. The amino acid number is indicated above the Leu to Phe mutation of TS48 (SEQ ID NO:12). The last line is a consensus sequence. The Leu residue is highly conserved. Genetic lesions of TS60 (SEQ ID NO:17) and corresponding residues are in bold. The amino acid numbers are indicated above the Glu to Lys and Ala to Val mutations of TS60 (SEQ ID NO:17). Boxed residues correspond to the HS 33 mutation (SEQ ID NO:1) previously identified and shown to be important in heat stability of the maize endosperm AGP. The last line is a consensus sequence.

Figures 5A and 5B show molecular characterization of RTS 48-2 (SEQ ID NO:27) and RTS 60-1 (SEQ ID NO:32), respectively. Genetic lesion of RTS 48-2 (SEQ ID NO:27) and corresponding residues are in bold. The amino acid number is indicated above the Ala to Val mutation of RTS 48-2 (SEQ ID NO:27). The last line is a consensus sequence. Of significance, the mutation identified in RTS 48-2 (SEQ ID NO:27) maps to the identical residue found in the heat stable variant HS13. HS 13 contained an Ala to Pro mutation at position 177. Genetic lesion of RTS 60-1 (SEQ ID NO:32) and corresponding residues are in bold. The amino acid number is indicated above the Ala to Val mutation of RTS 60-1 (SEQ ID NO:32). The last line is a consensus sequence.